

FIG.1

A

AAAATGGTCCTTCTGTTGATCCTGTGAGTCTTACTTTTGAAAGAAGATGT
 CCGTGGGAGTGCACAGTCCAGTGAGAGGAGGGTGGTGCGTCACATGCTGG
 GTGACATCATTATTGGAGCTCTCTTTCTGTTTCATCACCAGCCTACTGTG
 GACGAAGTTTCATGAGAGGAAGTGTGGGGCAGTCCCGTGAACAGTATGGCAT
 TCAGAGAGTGGAGGCCATGCTGCATACCTGGAAGGATCAATTACAGACC
 CCACACTCTTGCCCAACATCACACTGGGCTGTGAGATAAGGGATTCTCTGC
 TGGCATTTCGGCTGTGGCCCTAGAGCAGAGCATTGAGTTCATAAGAGATTC
 CCTCATTTCTTCGGAAGAGGAAGAGGGCTTGGTATGCTCTGTGGATGGCT
 CCTCCTCTTCTTCCGCTCCAAGAAGCCCATAGTAGGGGTCAATGGGGCT
 GGTTCAGTTCTTTAGCCATTAGGTCCAGAATTTGCTCCAGCTTTTCAA
 CATACCTCAGATTGCTTACTCAGCAACCATCATGGATCTGAGTGACAAGA
 CTCTGTTCAAATATTTTCATGAGGGTTGTGCCTTCAGATGCTCAGCAGGCA
 AGGTCCATGGTGGACATAGTGAAGAGGTACAACCTGGACCTATGTATCAGC
 CGTACACACAGAAGGCAACTATGGAGAAAGTGGGATGGAAGCCTTCAAAG
 ATATGTCAGCGAAGGAAGGGATTGTCATCGCCCACTCTTACAAAATCTAC
 AGTAATGCAGGGGAGCAGAGCTTTGATAAGCTGCTGAAGAAGCTCACAAG
 TCACCTTGCCCAAGGCCCGGTGGTGGCCTACTTCTGTGAGGGCATGACGG
 TGAGAGGTCTGCTGATGGCCATGAGGCGCCTGGGTCTAGTGGGAGAAATTT
 CTGCTTCTGGGCAGGGAACAGATGCCATCTTTATTGAGATCTCAAAGAA
 CAGCATCCTATGGAAGACAGAAGAAAATGCCAAGTGCCTCTCTTCAGG
 GTTTTGAGACATATTACACAGAAGTGAGTCCGTGCTGCTGCACATGCC
 CAGCCTCTGAATCTAGAGCTCAGTTCAGGGCCCATCACTGGACTGAGGGA
 CAGGCTCATCTAATCTGAGTGGATATTACTCTGCATTATAATGAAGCA
 ACAGTCATATCTTCTGATGTGGAGATTGAGAAGCATTGTATTGGATGT
 GACCGTCAAATGCGCCCATATCACTGCAACACCTACAAGTTTCTTGC
 ATGGGTGCTCAGACTTTCACCTCTGGCAAGTATTACTGGGAGGTCCATG
 TGGGGGACTCTTGAATTTGGGCTTTCGGTGTTTGAATAAGTACTGGAAA
 GGGAGAATCAGAATGGCAATATATATGAGAGGAGGGGACTCTTTAGTCT
 TGGGATTGTTAAGAACGACATTCAGTGCAGTCTCTTTACCACTCCCGAG
 TTACACTGCAGTATGTCCCAAGACCTACCAACCATGTAGGATTATCTCTG
 GATTGTGAAGCTAGAAGTGTGAGCTTCGTTGATGTTAATCAAAGCTCCCC
 TATATACACCATCCCTAATTGCTCCTTCTCACTCCTCTCAGGCCATCT
 TTTGCTGTATTCATCTCTGACCAGAGACAAATCAGAAATGTGTTTATCTG
 CTGTGGGAACCCCTTTATCCCAATAAGCCCTCTCTCTGTGCCTTATCAA
 ACAGGACAAATAGGTTCTGTTTTATGCTTGAATTGCATTCTAATGTTAT
 TAAAACCTATTTATTGTGTTACTATTAAATGTGGTAAAMCACAACAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

B

MVLILLISVLLLLKEDVRGSAQSSERRVVHMLGDIIGALFSVHHQPTVDVEVHERKCGAV
 REQYGIQRVEAMLHTLERINSDPTLLPNITLGCIEIRDSCHWSAVALEQSIEFIRDSLSS
 EEEGLVCSVDGSSSSFRSKKPIVGVIGPGSSSLAIQVQNLQLFNIPQIAYSATIMDLS
 DKTILFYFMRVVPDSDAQQARSMVDIVKRYNWTYVSAVHTEGNYGESMEAFKDMSAKEGI
 CIAHSYKIYSNAGEQSFDKLLKKLTLHLPKARVVAYFCEGMTVRGLMAMRRLGLVGEFL
 LLGREPDPAIFIEISKNSILWEDRRKQGRFLQGFGDILHRSESVLLHMPQPLNLELSSGP
 ITGLRDRLI

FIG.2

Alignment of:
Sequence Start End Sequencetype

rat1-369 (1 > 369) PROTEIN
mGluR5M (1 > 369) PROTEIN
human1-370 (1 > 370) PROTEIN

1 60
rat1-369 MVLLILSVLLLKEDVRGSAQSSERRVVAHMPGDIIIGALFSVHHQPTVDKVERKCGAV
mGluR5M MVLLILSVLLLKEDVRGSAQSSERRVVAHMLGDIIIGALFSVHHQPTVDEVHERKCGAV
human1-370 MVLLILSVLLLKEDVRGSAQSSERRVVAHMPGDIIIGALFSVHHQPTVDKVERKCGAV

61 120
rat1-369 REQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSVALEQSIIEFIRDSLSS
mGluR5M REQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSVALEQSIIEFIRDSLSS
human1-370 REQYGIQRVEAMLHTLERINSDPTLLPNITLGCEIRDSCWHSVALEQSIIEFIRDSLSS

121 180
rat1-369 EEEGLVRCVDGSSS-FRSKKPIVGVIGPGSSSVAIQVQNLQLFNI PQIAYSATSMDSL
mGluR5M EEEGLVCSVDGSSSFRSKKPIVGVIGPGSSSLAIQVQNLQLFNI PQIAYSATIMDSL
human1-370 EEEGLVRCVDGSSSFRSKKPIVGVIGPGSSSVAIQVQNLQLFNI PQIAYSATSMDSL

181 240
rat1-369 DKTLFKYFMRVVPDAQQARAMVDIVKRYNWTYVS AVHTEGNYGESGMEAFKDMSAKEGI
mGluR5M DKTLFKYFMRVVPDAQQARSMVDIVKRYNWTYVS AVHTEGNYGESGMEAFKDMSAKEGI
human1-370 DKTLFKYFMRVVPDAQQARAMVDIVKRYNWTYVS AVHTEGNYGESGMEAFKDMSAKEGI

241 300
*
rat1-369 CIAHSYKIYSNAGEQSFDKLLKKLRSHPKARVVACFCEGMTVRGLLMAMRRLGLAGEFL
mGluR5M CIAHSYKIYSNAGEQSFDKLLKKLTSHPKARVVAYFCEGMTVRGLLMAMRRLGLAGEFL
human1-370 CIAHSYKIYSNAGEQSFDKLLKKLTSHPKARVVACFCEGMTVRGLLMAMRRLGLAGEFL

301 360
rat1-369 LLGSDG-----WADRYDVT DGYQREAVGGITIKLQSPDVKWFDDYYLKLRL--
mGluR5M LLGREPDAIFIEISKNSILWEDRRKCQGRFL-QGFGDILHRSESVLLHMPQLNLLESSLG
human1-370 LLGSDG-----WADRYDVT DGYQREAVGGITIKLQSPDVKWFDDYYLKLRL--

361 385
rat1-369 PETNLRNPWFQEFWQHRFQCRLEGF
mGluR5M PITGLRD-----RL--I
human1-370 PETNHRNPWFQEFWQHRFQCRLEGF